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Axel ULLRICH et al.  
DNA ENCODING MCK-10, A NOVEL  
RECEPTOR TYROSINE  
Atty. Dkt. No. 034536-0447  
SN 09/551,188

1 CCGGCCCTGAGACTTGGGGTGA  
 61 CTGCTCTCGGGAGCCGCCTCCGACACCGAGCCCCGGCTCCGGCT  
 121 CGGGCTTCTGGCTCCGCTTCCCCCGCCCTGGGGCGGGCT  
 181 CCCGGGTGGGACTGGCTTGCCGGATGAGGGTGTCTGA  
 241 TCACTGAGCGATTGGGACTTGAAGGAATGCCAAGAGATGCTG  
 CCGGGCCCCGACAG  
 CCCCCGGCTCCGGCT  
 AGGGGGGGGGCT  
 AGGGGGGGGGCT  
 GGGGGGGGGGGCT

1	M G P E A L S S L L L L L L
301	GGCCCGAGGGATCAGGAGCTATGGGACCATGGCCCTGTCACTTACTGCTGCTGCTCT
15	V A S G D A D M K G H F D P A K C R Y A
361	TGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTGATCCAGCAACTGACATCTGCTTCAGGCTCCTGGT
35	L G M Q D R T I P D S D I S A S S S W S
421	CCCTGGCATGCAGGACCGAACATCCCAGACAGTGA
55	D S T A A R H S R L E S S D G D G A W C
481	CAGATTCCACTGCCGCCACAGCACGGTGGAGAGCAGTGACGGGATGGGGCTGCTGGT
75	P A G S V F P K E E Y L Q V D L Q R L
541	GCCCCGAGGGTGGTGGTTCCAAGGAGGGAGTACTGCAAGTGGATCTACAAAGCAC
95	H L V A L V G T Q G R H A G G L G K E F
601	TCCACCTGGTGGCTCTGGTGGCACCCAGGGACGGCATGGGGCCTGGGCAAGGAGT

FIG. 1A



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DNA ENCODING MCK-10, A NOVEL  
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115    S   R   S   Y   R   L   R   Y   S   R   D   G   R   R   W   M   G   W   K   D  
661    TCTCCCGGAGCTACCCGGCTTACTCCCGGATGGCTGGCTGGATGGCTGGAGG

135    R   W   G   Q   E   V   I   S   G   N   E   D   P   E   G   V   V   L   K   D  
721    ACCGGCTGGGGTCAGGAGGTGATCTCAGGCCAATGAGGAACCCCTGAGGGAGTGCTGGCTGAAGG

155    L   G   P   P   M   V   A   R   L   V   R   F   Y   P   R   A   D   R   V   M  
781    ACCTTGGCCCCCATGGTTGCCGACTGGCTCTACCCCCGGCTGACCGGGTCA

175    S   V   C   L   R   V   E   L   Y   G   C   L   W   R   D   G   L   L   S   Y  
841    TGAGTGTCTGTCTGGGTAGAGCTCTATGGCTGCCCTCTGGAGGGATGGACTCCTGTCTT

195    T   A   P   V   G   Q   T   M   Y   L   S   E   A   V   Y   L   N   D   S   T  
901    ACACCCGCCCTGTGGGCAGACAATGTATTATCTGAGGCCGTGTACCTAACGACTCCA

215    Y   D   G   H   T   V   G   G   L   Q   Y   G   G   L   G   Q   L   A   D   G  
961    CCTATGACGGACATAACCGTGGGGACTGCAGTATGGGGTCTGGCCAGCTGGCAGATG

235    V   V   G   L   D   D   F   R   K   S   Q   E   L   R   V   W   P   G   Y   D  
1021    GTGTGGCTGGGTGACTTAGGAAGAGCTCAGGAGCTGGCTATGTGGAGATGGAGTTGAGT

255    Y   V   G   W   S   N   H   S   F   S   S   G   Y   V   E   M   E   F   E   F  
1081    ACTATGTGGCATGGAGCAACCACAGCTTCCAGTGGCTATGTGGAGATGGAGTTGAGT

FIG. 1B



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275    D R L R A F Q A M Q V H C N N M H T L G  
1141    TTGACCGGGCTGAGGGCCTTCAGGCCATGCAAGGTCCACTGTAACAAACATGCACACGCTGG  
  
295    A R L P G G V E C R F R R G P A M A W E  
1201    GAGCCCCGTCTGGCCTGGGAATGTCGGCTTCCGGGACTGGCCATGGCCTGGCTGG  
  
315    G E P M R H N L G G N L G D P R A R A V  
1261    AGGGGGAGGCCATGCCAACCTAGGGGAAACTGGGACCCCAGAGCCCCAG  
  
335    S V P L G G R V A R F L Q C R F L F A G  
1321    TCTCAGTGCCCCCTTGCGGGCGTGTGGCTCGCTTCTGCAGTGCCGCTTCCTTGCGG  
  
355    P W L L F S E I S F I S D V V N N S S P  
1381    GGGCCCTGGTTACTCTTCAGGAAATCTCTTCATCTGTAATTCCTCTC  
  
375    A L G G T F P P A P W W P P G P P T N  
1441    CGGCACCTGGAGGCACCCCTTCGGCCAGGGCCAGGGCCCTGGCACCTCCCCACCA  
  
395    F S S L E L E P R G Q Q P V A K A E G S  
1501    ACTTCAGCAGGCCATCCTGGAGCTGGAGCCAGGGCCAGGCCAGGGCAAGGCCAGGGGA  
  
415    P T A I L I G C L V A I I L L L L I I  
1561    GCCCGACCGCCATCCTCATCGGCTGGCTGGCCATCATCCTGCTGCTCATCA

FIG.1C



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435    A L M L W R L H W R R L L S K A E R R V  
1621 TTGCCCTCATGCTCTGGGGCTGCAC TGCGGCAGGGCTCCTAGCAAGGCTGAACGGAGGG

455    L E E E L T V H L S V P G D T I L I N N  
1681 TGTGGAAAGAGGAGGCTGACGGTTCACTCTGTCCCTGGGGACACTATCCTCATCAACA

475    R P G P R E P P Y Q E P R P R G N P P  
1741 ACCGCCAGGT CCTAGAGGGCCACCCCCGTACCGAGGGAGCCCTCGTGGAAATCCGC

495    H S A P C V P N G S A L L L S N P A Y R  
1801 CCCACTCCGGCTCCCTGTGTCCTAACATGGCTCTCGCTGCTCCAAATCCAGGCTTACCC

515    L L L A T Y A R P P R G P G P P T P A W  
1861 GCCTCCCTCTGCCACTTA CGCCCTTGAGGGCCCCCACACCCGGCT

535    A K P T N T Q A Y S G D Y M E P E K P G  
1921 GGGCAAACCAACCAACCCCCAGGCCTACAGTGGGACTATATGGAGGCCTGAGAACCCAG

555    A P L L P P P Q N S V P H Y A E A D I  
1981 GGGCCCGCTCTGCCCTACCTCCCCAGAACAGGCTCCATTATGCCAGGGCTGACA

575    V T L Q G V T G G N T Y A V P A L P P G  
2041 TTGTTACCCCTGCAGGGCTCACCGGGCAACACCCATTATGCTGTGCACTGCCAG

FIG. 1D



595    A    V    G    D    G    P    P    R    V    D    F    P    R    S    R    L    R    F    K    E  
2101    GGGCAGTCGGGATGGCCCCCAGAGTGGATTCCCTCGATCTGACTCGCTCGTTCAAGG

615    K    L    G    E    G    Q    F    G    E    V    H    L    C    E    V    D    S    P    Q    D  
2161    AGAAGCTTGGCAGGGCCAGTTGGGAGGTGCACCTGAGCTGACAGGCCCTCAAGG

635    L    V    S    L    D    F    P    L    N    V    R    K    G    H    P    L    L    V    A    V  
2221    ATCTGGTCAGTCTTGATTCCCCCTTAATGTCGTAAGGGACACCCTTGTGCTGGTAGCTG

655    K    I    L    R    P    D    A    T    K    N    A    S    F    S    L    F    S    R    N    D  
2281    TCAAGATCTTACGGCCAGATGCCACCAAGAAATGCCAGCTTCCTTGTTCTCCAGGAATG

675    F    L    K    E    V    K    I    M    S    R    L    K    D    P    N    I    I    R    L    L  
2341    ATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCAAGGACCCAACATCATTCGGTAGC

695    G    V    C    V    Q    D    D    P    L    C    M    I    T    D    Y    M    E    N    G    D  
2401    TGGGGTGTGAGGACGGACCCCTCTGCATGATTACTGACTACATGGAGAACGGCG

715    L    N    Q    F    L    S    A    H    Q    L    E    D    K    A    A    E    G    A    P    G  
2461    ACCTCAACCAGTTCCCTCAGTGGCCCACCAAGCTGGAGACAAGGGCAGGGGGCCCTG

735    D    G    Q    A    A    Q    G    P    T    I    S    Y    P    M    L    L    H    V    A    A  
2521    GGGACGGGCAGGGCTGGCAGGGCCACCATCAGCTACCCAAATGCTTGCTATGTGGCAG

FIG. 1E



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755 Q I A S G M R Y L A T L N F V H R D L A  
2581 CCCAGATCGCCTCCGGCATGGCTATCTGGCACACTCAACTTGTACATCGGACCTGG

775 T R N C L V G E N F T I K I A D F G M S  
2641 CCACGGAAACTGCCTAGTTGGGAAATTTCACCATAAAATCCGAGACTTGGCATGA

795 R N L Y A G D Y R V Q G R A V L P I R  
2701 GCCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGGGCAGTGTGCCATCC

815 W M A W E C I L M G K F T T A S D V W A  
2761 GCTGGATGCCCTGGAGTGCACTCCTCATGGGAAGTTACGACTGGGAGGTGACGTGTGGG

835 F G V T L W E V L M L C R A Q P F G Q L  
2821 CCTTGTGTGACCCCTGTGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCCAGGCAGC

855 T D E Q V I E N A G E F F R D Q G R Q V  
2881 TCACCGACGAGCAGGTCACTGGAGAACGGGGAGATTCCTGGGACCCGGGGCAGG

875 Y L S R P P A C P Q G L Y E L M L R C W  
2941 TGTACCTGTCCGGCCCTGGCTGGGGCAAGGGCTATATGAGCTGATGCTTCGGTGCCT

895 S R E S E Q R P P F S Q L H R F L A E D  
3001 GAGCCGGAGGTCTGAGGAGCCACCCCTTTCCAGCTGGCATCGGTCTGGCAGAGG

FIG. 1F



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RECEPTOR TYROSINE  
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915    A L N T V  
3061 ATGCACCTAACACACGGTGTGAATCACACATCCAGGCTGCCCTCAGGGAGTGATCCAG

3121    GGGAAAGCCAGTGACACTAAACAAGAGGACACAATGGCACCTCTGCCCTTCCCCTCCCGA  
3181    CAGCCCCATCACCTCTTAATAGAGGCAGTGAGACTGCAAGCTGGACACACTCTCATGTC  
3241    CTGATGCCCTCTCCCTCTGGACACACTCTCATGTCGCCCTGGATGGATCCACCCCTCT  
3301    TAGAAGGCCCTGGGAAAGGGTGGAGAAATAAGGATAGACACTGGACATGCCCATTT  
3361    AGCCATCCCTGGGAAAGGGTGGAGAAATAAGGATAGACACTGGACATGCCCATTT  
3421    GAGCACCTGGCCCCACTGGACAAACACTGATTCCTGGAGGGTGGCTGGCCCAAGCTTC  
3481    TCTCTCCCTGTACACACTGGACCCACTGGCTGAGAATCTGGGGTGGAGGACAAGA  
3541    AGGAGAGGAAATGTTCCCTGGCCTGCTGTACTTGTACTTGTACTTGGCTTCTTC  
3601    CTCCTCCATCACCTGAAACACTGGACCTGGGGTAGGCCCAAGCCCTCAGTCACCC  
3661    CCACTTCCCACCTTGAGCTTGAACCTTGAGCTTGAACCTCTAAGCCTATACGTT  
3721    TAAATATTGGGATTGGGGAAAGAGGGAGCAACGGGGCATAGCCCTGGGGTGGACATC  
3781    TCTAGTGTAGCTGCCACATTGATTCTATAATCACTTGGGTTGTACATTGGGG  
3841    GGAGAGACACAGATTACACTAATATGGACCTAGCTTGAGGCAATTAACTCCCT  
3901    GCACTAGGCAGGTAATAAAAGGTGAGTTCCACAAAAAAACGGAAAT  
3961    TC

FIG. 1 G

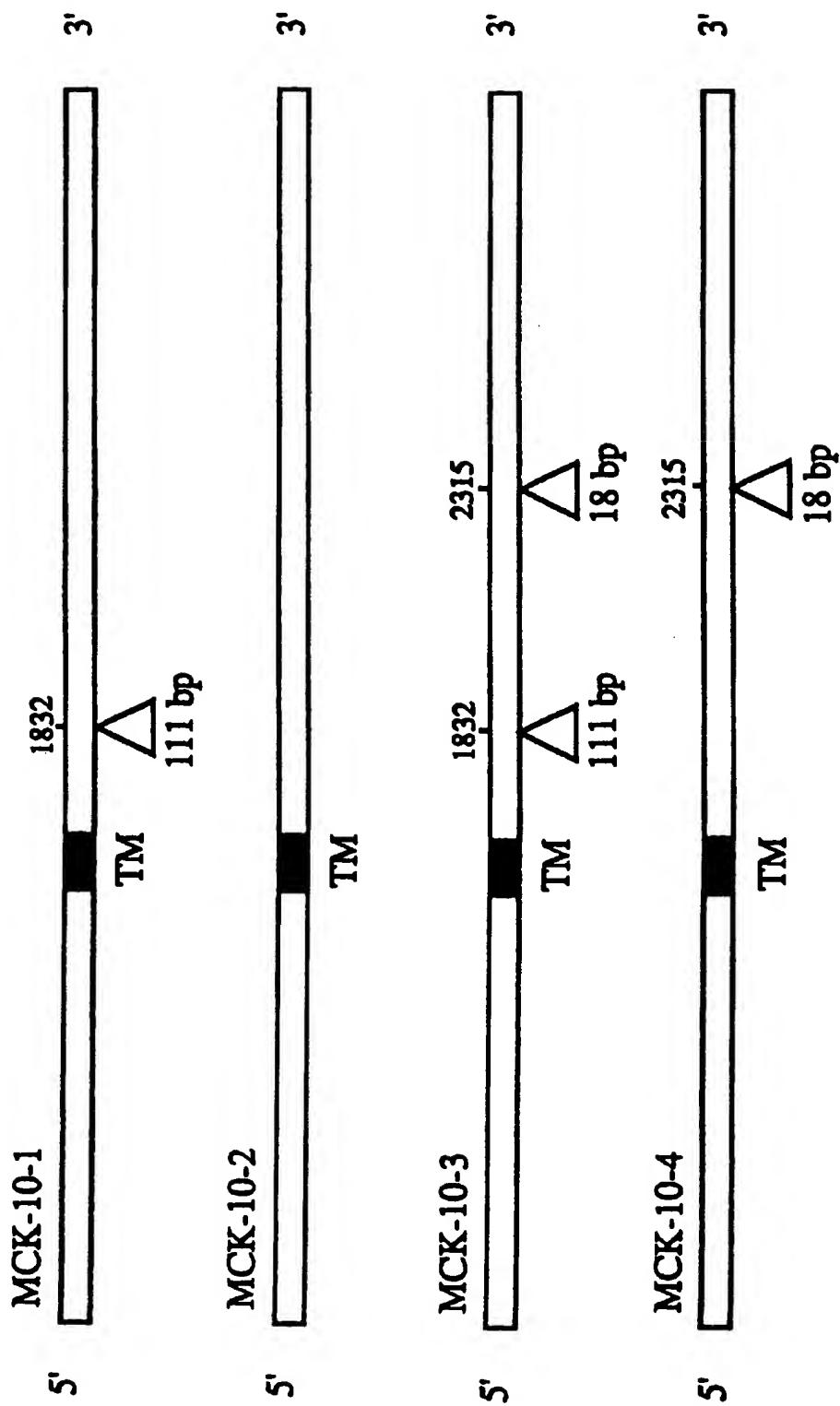


FIG. 2



	gcacgagcggcacgagtcctgtatgtttttccatccccccttccgttgtctacttct	61
2	cgtgttcggcggtgttcggatcgatcgatggaaaggtagggggaaaggatccgtgtgg	-
b	tttcttgctcatcttggatcgatgtgtcaatccccatataatccatccatccatccat	-
62	aaatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	121
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-
122	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	181
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-
182	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	241
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-
242	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	301
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-
302	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	361
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-
362	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	421
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-
	H I L I P R M L L V L F L L L P I	-
422	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	481
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-
482	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	541
b	ttatccatccatccatccatccatccatccatccatccatccatccatccatccatccat	-

FIG.3A



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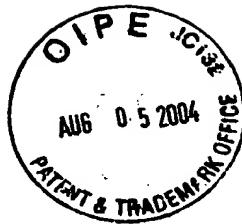
**FIG. 3B**



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DNA ENCODING MCK-10, A NOVEL  
RECEPTOR TYROSINE  
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962	GCTGGGCACCAAGTTGACTCCCTGGAGGTCCATCATTATCTGAATGATTCTGTCTAT CGACCCGTCGTAAACATGAGGGACCTCCAAGGTAGTAAATAGACTTACTAAGACAGATA	1021
b	A G Q Q F V L P G G S I I Y L N D S V Y -  GATGGAGCTGTTGGATACAGCATGACAGAAGGGCTAGGCCATTGACCGATGGTGTCT	
1022	CTACCTCGACAACCTATGTCGTACTGTCTTCCCATTCCGTTAACGGCTACCACACAGA	1081
b	D G A V G Y S M T E G L G Q L T D G V S -  GCCCTGGACGATTCACCCAGACCCATGAATACCAACGTGTGGCCCGCTATGACTATGTG	
1082	CCGGACCTGCTAAAGTGGCTCTGGTACTTATGGTGACACCGGGCCGATACTGATAACAC	1141
b	G L D D F T Q T H E Y H V W P G Y D Y V -  GGCTGGCCCAACGAGACTGCCACCAATGGCTACATTGAGATCATGTTGAATTGACCGC	
1142	CCGACCCGCTTGCTCTCACCGTGCTTACCGATGTAACTCTAGTACAAACTAAACTGGCG	1201
b	G W R N E S A T N G Y I E I M F E F D R -  ATCAGGAATTCACTACCATGAAGGTCCACTGCAACAAACATGTTGCTAAAGGTGTGAAG	
1202	TAGTCCTTAAACTGATGGTACTTCCAGGTGACGTTGTTGACAAACGATTCCACACTTC	1261
b	I R N F T T M K V H C N N M F A K G V K -  ATCTTTAAGGAGGTACAGTGCCTACTTCCGCTCTGAAGCCAGTGACTGGTACCTAATGCC	
1262	TAGAAATTCCCTCATGTCACGATGAAGGCGAGACTTCCGTCACTCACCCATGGATTACGG	1321
b	I F K E V Q C Y F R S E A S E W V P N A -  ATTTCCCTcccccttgtcctggatgacgtcaaccccgatgcgtcggttgtcacgggtgcct	
1322	TAAAGGAAGggggaoacaggccactgcaagllggggcacgagccaaacoglgccacggaa	1381
b	I S F P L V L D D V N P S A R F V T V P -	

FIG.3C



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FIG.3D



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	cgccctgactacCAGGAGCCATCCAGGCTGATACGAAAACCTCCAGAATTGCTCCAGGG	1861
1802	gcgggactgtgGTCTCGGTAGGTCCGACTATGCTTTGAGGTCTTAAACGACGTCCC	
b	R P D Y Q E P S R L I R K L P E F A P G	-
	GAGGAGGAGTCAGGCTCCAGCGGTGTTGAAGCCAGTCCAGCCCAGTGGCCCTGAGGG	1921
1862	CTCCTCCTCAGTCCGACGTCCCCACAACACTTCGGTCAGGTGGTCAACGGGACTCCCC	
b	E E E S G C S G V V K P V Q P S G P E G	-
	GTGCCCCACTATGCAGAGGCTGACATACTGAACCTCCAAGGAGTGACAGGAGGAAACACA	1981
1922	CACGGGGTGTACGTCTCGACTGTATCACTGGAGCTTCCCTACTGTCCCTCGTTGT	
b	V P H Y A E A D I V K L Q G V T G G N T	-
	TACTCAGTGCCTGCCCTCACCATGGACCTGCTCTCAGGAAAACATGTGGCTGTGGAGGAG	2041
1982	ATGAGTCACGGACGGCAGTGGTACCTGGACGAGTCCTTCTACACCGACACCTCCTC	
b	Y S V P A V T M D L L S G K D V A V E E	-
	TTCCCCAGGAAACTCTAACTTCAAAGACAAGCTGGAGAAGGACAGTTGGGAGGTT	2101
2042	AAGGGTCTTGGAGGATTGAAAGTTCTCTCGACCCCTTCCGTCAAACCCCTCCAA	
b	F P R K L L T F K E K L G E G Q F G E V	-
	CATCTCTGTGAAGTGGAGGAAATGAAAAATTCAAAGACAAGATTTGCCCTAGATGTC	2161
2102	GTAGAGACACTTCACCTCCCTAACCTTTTAAGTTCTGTTCTAAACGGGATCTACAG	
b	H L C E V E G M E K F K D K D F A L D V	-
	ACTGCCAACCAACCAGCCTGCTGGCTGTGAAAATGCTCCGAGCAGATGCCAACAGAAT	2221
2162	TCACGGTTGGTGGACAGGACCCACCGACACTCTACCGAGGCTCGTACGGTTGTTCTTA	
b	S A N Q P V L V A V K M L R A D A N K N	-

FIG.3E

2222    GCCAGGAATGATTTCTTAAGGAGATAAACATCATGTCTGGCTAAGGACCCAAACATC    2281  
          CGGTCCCTACTAAAAGAATTCTCTATTTCTAGTACAGAGCCGAGTCCTGGTTGTAG  
  
b    A R N D F L K E I K I M S R L K D P N I    -  
  
2282    ATCCATCTATTAGCTGCTGTATCACTGATGACCCCTCTCTGTATGATCACTGAATAACATC    2341  
          TAGGTAGATAATCGACACACATAGTCACTACTGGAGAGACATACTACTGACTTATGTAC  
  
b    I H L L A V C I T D D P L C M I T E Y M    -  
  
2342    GAGAATGGAGATCTCAATCAGTTCTTCCCCCACGAGCCCCCTAATTCTCCTCCAGC    2401  
          CTCTTACCTCTAGACTTAGCTCAAAGAAAGGGCGTGCTCGGGGATTAAGAAGGAGGTCG  
  
E N G D L N Q F L S R H E P P N S S S S    -  
  
2402    GATGTACCGACTGTCAGTTACACCAATCTGAAGTTATGGCTACCCAAATTGCCTCTGGC    2461  
          CTACATGGTGACAGTCATGTGTTAGACTCAAATACCGATGGTTAACGGAGACCG  
  
b    D V R T V S Y T N L K F M A T Q I A S G    -  
  
2462    ATGAAGTACCTTCCTCTTAATTTGTTACCGAGATCTGCCACACGAAACTGTTA    2521  
          TACTTCATGCAAACGAGAGAATTAAAACAAGTGGCTCTAGACCGGTGTCCTTGACAAAT  
  
b    M K Y L S S L N F V H R D L A T R N C L    -  
  
2522    GTGGGTAAAGAACTACACAATCAAGATAGCTGACTTTGGAATGAGCAGGAACCTGTACAGT    2581  
          CACCCATTCTTGATGTGTTAGTTCTATCGACTGAAACCTTACTCGTCCTGGACATGTCA  
  
b    V G K N Y T I K I A D F G M S R N L Y S    -  
  
2582    GCTGACTATTACCGGATCCAGGGGGGGGAGTGCTCCCTATCCGCTGGATGTCCTGGGAC    2641  
          CCACTGATAATGCCCTAGTCCCCGGCGTCACGAGGGATAGGGGACCTACAGAACCTC  
  
b    G D Y Y R I Q G R A V L P I R W M S W E    -

FIG.3F



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	AGTATCTGCTGGCAAGTTCACTACAGCAAGTGATGTGGCCCTTGGGTTACTTG		
2642	<u>                                                                  </u>		2701
	TCA TAGA AC GAC CC GT CA AGT GA TG CG TT CA CT AC AC ACC GG AA ACC CC AA TG AA AC		
b	S I L L G K F T T A S D V W A F G V T L -		
	T G C G A G A C T T C A C C T T T G T C A A G A A C A G C C T A T T C C A G C T G T C A C A T G A A C A G G T T		
2702	<u>                                                                  </u>		2761
	A C C C T C T G A A A C T G G A A A A C A G T C T T G T C G G A T A A G G G T C G A C A G C T C A C T T G T C C A A		
b	W E T F T F C Q E Q P Y S Q L S D E Q V -		
	A T T C A G A A T A C T G G A G A G T T C T C C G A G A C C A A G G G A G G C A G A C T T A C C T C C T C A A C C A		
2762	<u>                                                                  </u>		2821
	T A A C T C T T A T G A C C T C T C A A G A A G G C T C T G G T T C C C T C C G T C T G A A T G G A G G G A C T T G G T		
b	I E K T G E F F R D Q G R Q T Y L P Q P -		
	G C C A T T T G C C T G A C T C T G T G T A A G C T G A T G C T C A G C T G C T G G A C A A G A G A T A C G A A G		
2822	<u>                                                                  </u>		2881
	C G G T A A A C A G G A C T G A G A C A C A T A T T C G A C T A C G G A G T C G A C G A C C T C T T C T A T G C T C		
b	A I C P D S V Y K L M L S C W R R D T K -		
	A A C C G T C C C T C A T T C C A A G A A A T C C A C C T T C G C T C C T C A A C A A G G G C A C C G A G T G A T G C		
2882	<u>                                                                  </u>		2941
	T T G G C A G G G A C T A A G G T T C T T A G G T G C A A G A C G G A G G A C T T G T T C C G T G C T C A C T A C C		
b	N R P S F Q E I H L L L L Q Q G D E -		
	T G T C A G T G C C T G G C C A T G T T C C T A C G G C T C A G G T C C T C C T A C A A G A C C T A C C A C T C A C C		
2942	<u>                                                                  </u>		3001
	A C A G T C A C C G A C C G G T A C A A G G A T G C C G A G T C C A G G A G G G A T G T T C T G G A T G G T G A C T T G G		
b	C A T G C C T A T G C C A C T C C A T C T G G A C A T T A A T G A A A C T G A G A G A C A G A C C G T T G T T G C T		
3002	<u>                                                                  </u>		3061
	G T A C C G A T A C C G T G A G C T A G A C C T G T A A A T T A C T T G A C T C T C T G T C T C C G A A C A A A C C G A		

FIG. 3G



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b

3062      TTGCCCTCTTTCTGGTACCCCCACTCCCTACCCCTGACTCATATATACTTTTTTT  
              +-----+-----+-----+-----+-----+  
              AACGGGAGAAAGGACCAGTCGGGTGAGGGATGGGACTGACTATATGAAAAAAA 3121

b

3122      TTACATTAAAGAACTAAAAAAAAAAAAAGGGC  
              +-----+-----+  
              AATGTAATTCTTGATTTTTTTTTCCC 3158

b

FIG.3H

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1	MILIPRMILLVLFLLLPILSSA...KAQVNPAICRYPLGMSGQIPDEDIT	47 CCK-2
1	:     :      :   .   : .   :       :     .   .	
1	. . MPEALSSLLLLLVASGDAADMKGHDPAKCRYALGMQDRTIPDSDIS	48 MCK-10
48	ASSQWSESTAAKYGRILDSEEGDGAWCPEIPVEPDOLKEFLQIDLHTLHF	97
48	:       :     :         .     .   :     :     :	
49	ASSSWSDSTAARHSRLESSDGDGAWCAGSVFPKE.EEYLQVDLQLRLHLV	97
98	TLVGTQGRRAAGCHGIEFAPIMYKINYSRDGTRWI S W R N R H G K Q V L D G N S N P	147
98	.         :             .   :             :         .   :	
98	ALVGTQGRHAGGLKEFSRSYRLRYSRDGRWAGWKRDRHQEVISGNEDP	147
148	YDIFLKDLLEPPIVARFVRFIPVTDHSIIVCMRVELYGCWMLDGLVSYNAP	197
148	:       :     :         .   .   :     :         :       :	
148	EGWLIKDLGPPMVARLVRFYPRADRVMSVCLRVELYGCWLRDGLLSYTAP	197
198	ACQQFVLPGCSIIYLNDSVYDG.AVCYSMT EGLGQLTDGVSGLDDFTQTH	246
198	.     :   . :         .     :         .               ..	
198	VGQTMYLSEA..VYLNDSTYDGHTVGGLOYCGLGQLADGVWGLDDFRKSQ	245
247	EYHWPGYDYVGWRNESATNGYIEIMFEFDRIRNFITMKVHCNNMFAKGV	296
246	. :             .   .     :             .   .           .	
246	ELRWPGYDYVGWSNHSFSSGYVEMEFDFRLRAFAQAMQVHCNNMHTLGA	295
297	KIFKEVQC.YFRSEASEWVPNAISFPLVLDDVNPSARFVTVPVPLHHRMASA	345
296	:   :   :   :   .   .   :   .   :   :                   :	
296	RLPGGVECRFRRGPAWAEGEPMRHNLCCNLLGDPRARAVSVPLGGRVARF	345
346	IKCQYHFADTHMMFSEITFQSDAAMMNSEALPTS.....	380
346	:   .     :       .       :     .	
346	LQCRFLFAGPMLLFSEISFISD.WWNNSPALGGTFPPAPWWPPGPPPTN	394
381	....PMAPTTYDPMLKVDDSNTRILIGCLVAIIILLIAIVVILWROFWQ	426 TRANSMEMBRANE
395	..  .   . :   . :	
395	FSSLELEPRGQQPVAKAEGSPTAILIGCLVAIIILLLLITALMLWRLHMR	444 REGION
427	KMLEKASRRMLDDENTVSLSLPSDSSMFNNNRSSSPSEQGSNSTYDRIFP	476
445	:   .   . :   :       :   .   :	
445	RLLSKAERRVYLEEEELTVHLSVPGDTILINNRPGPREP.....	481

FIG.4A



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FIG.4B



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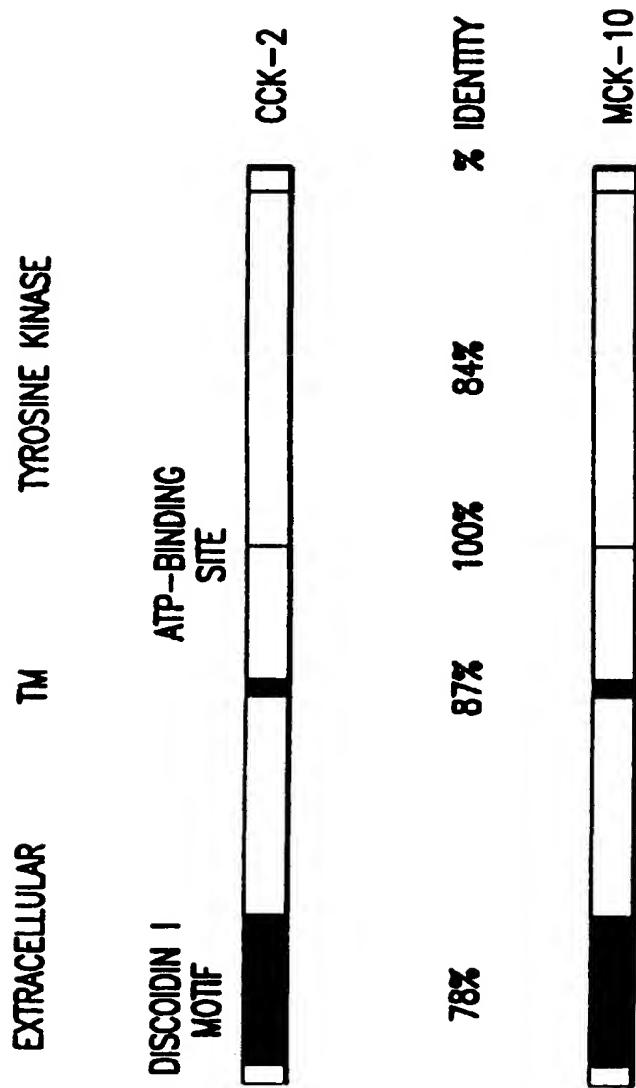


FIG. 4C



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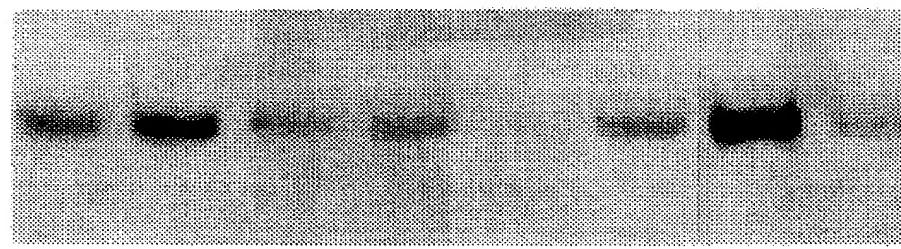
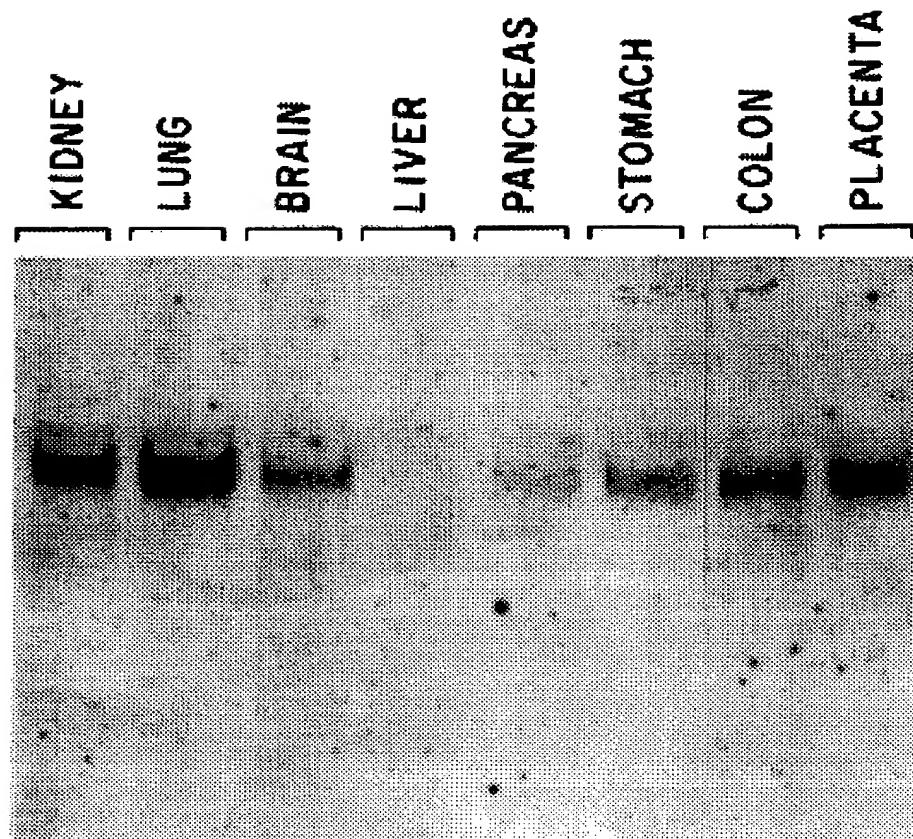
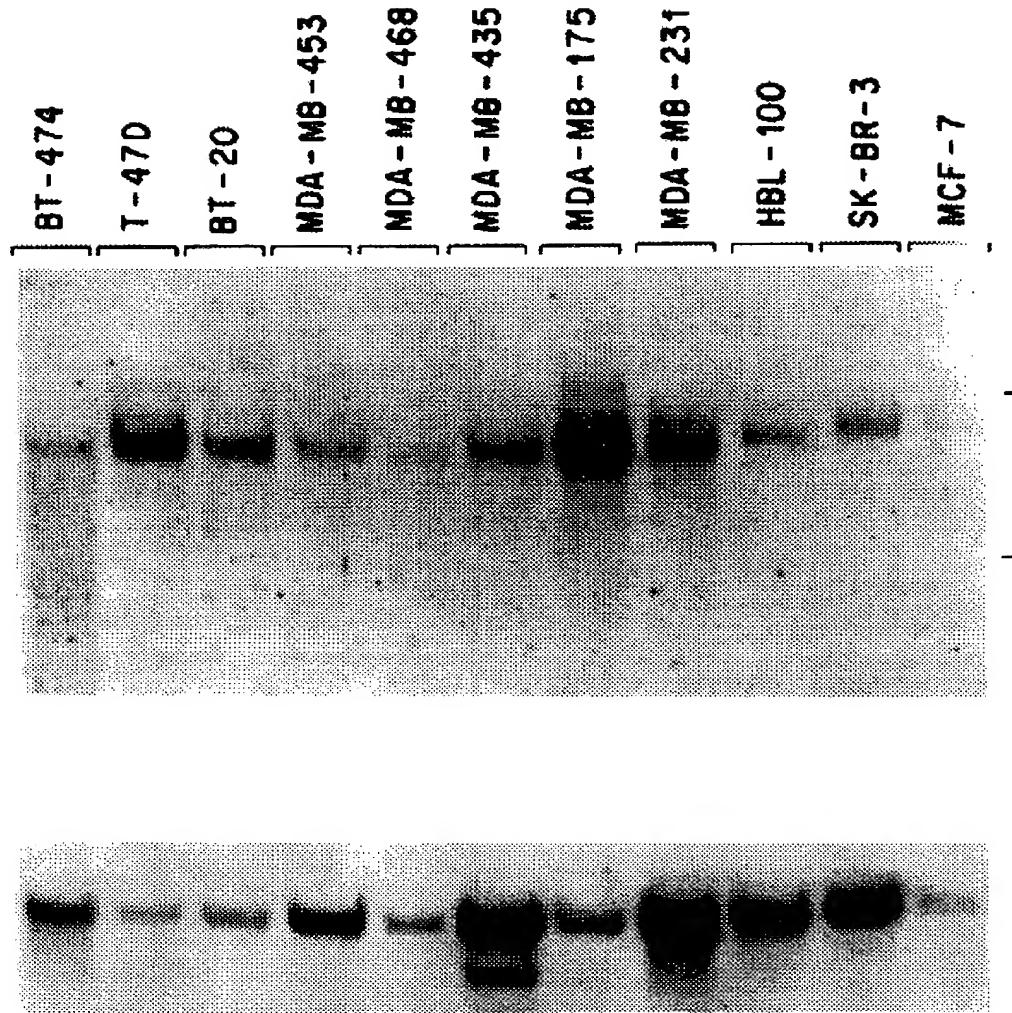


FIG.5A

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**FIG.5B**



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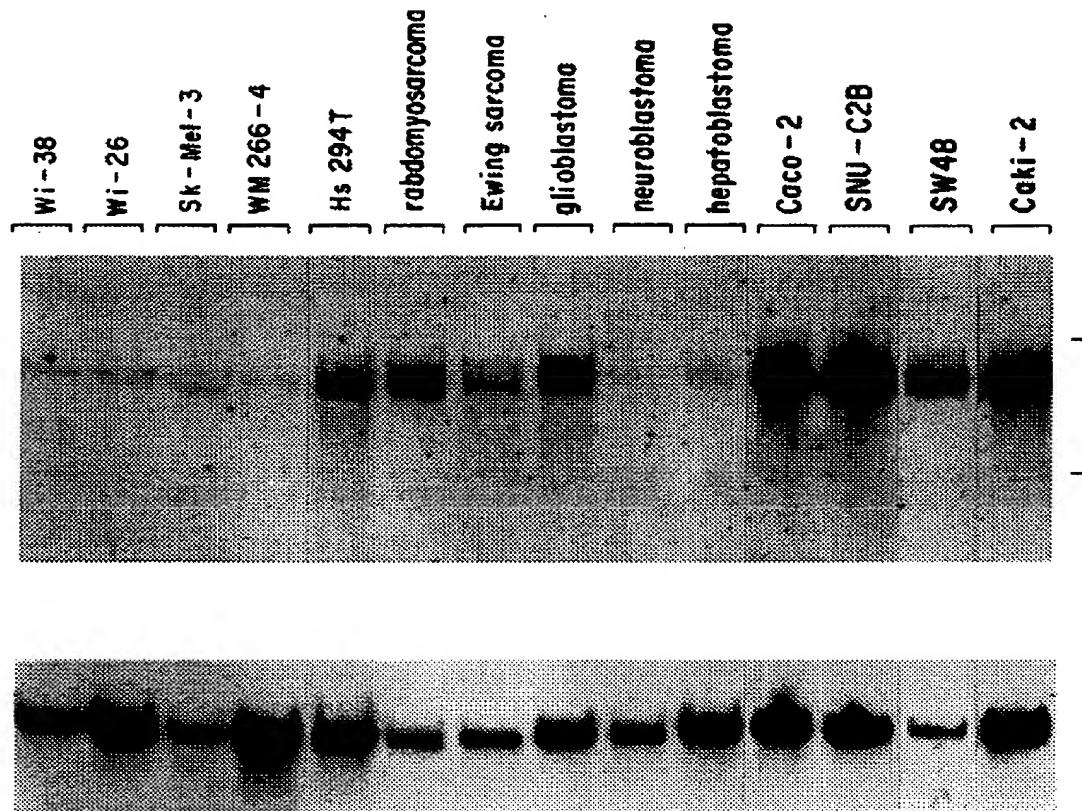


FIG.5C

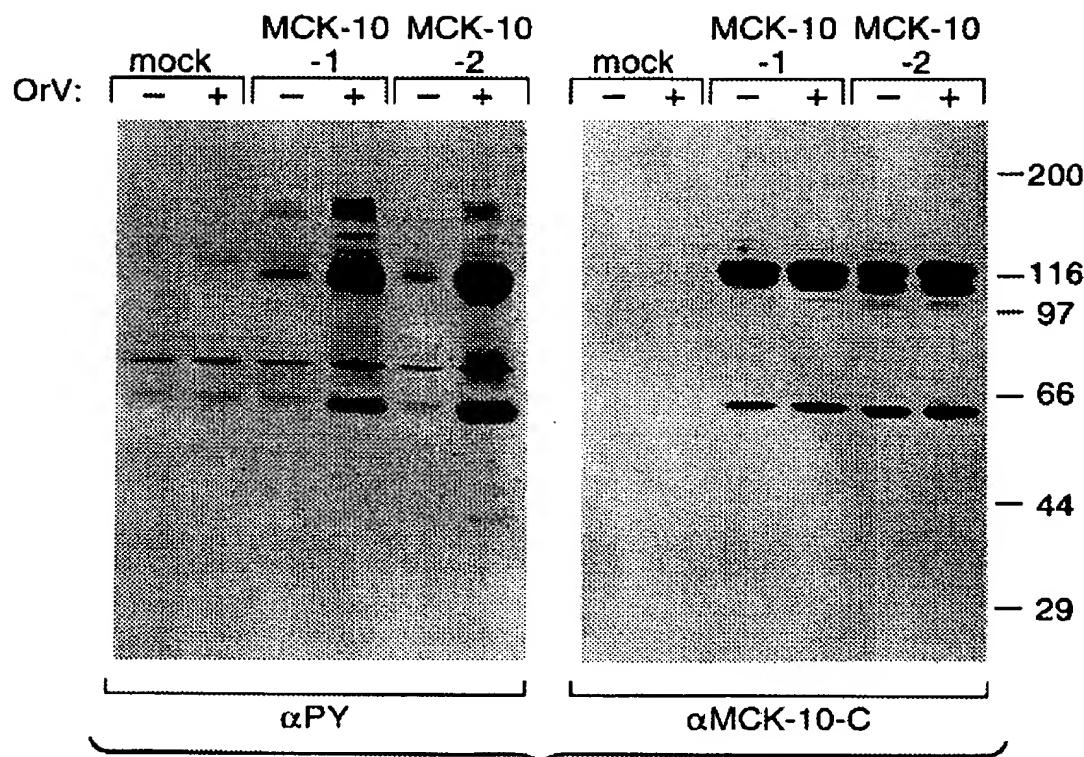


FIG.6A



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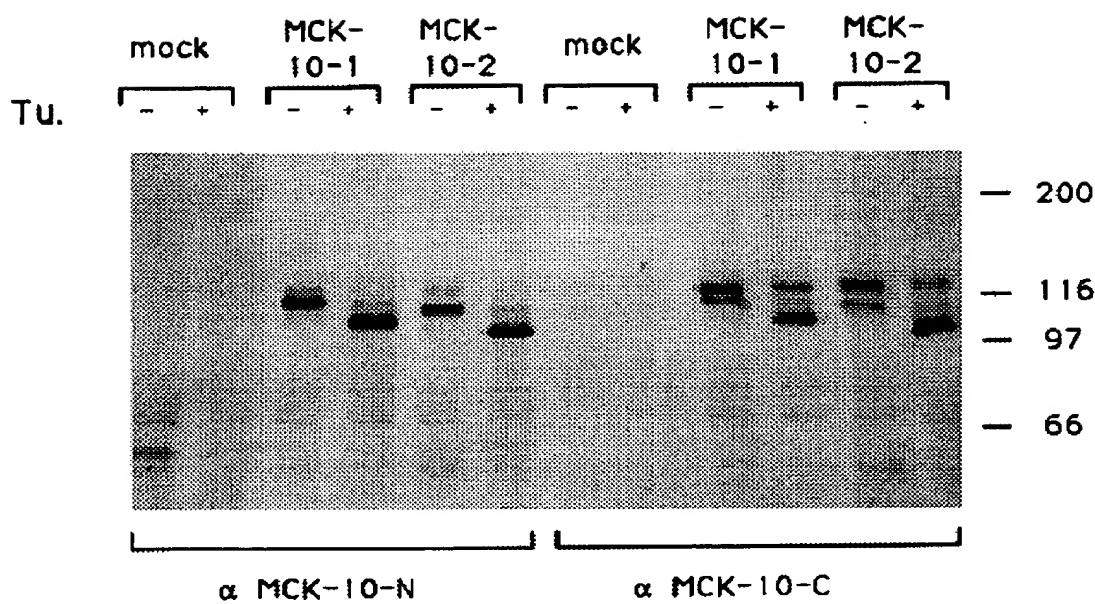


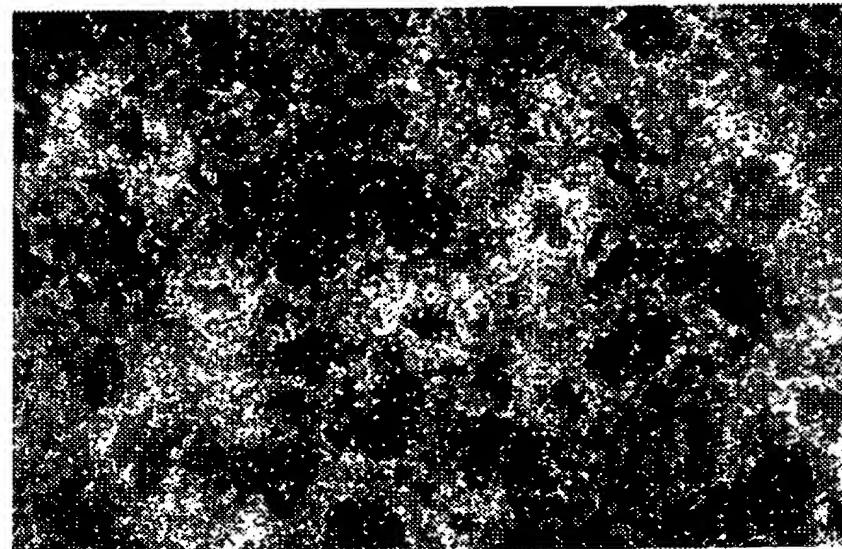
FIG.6B

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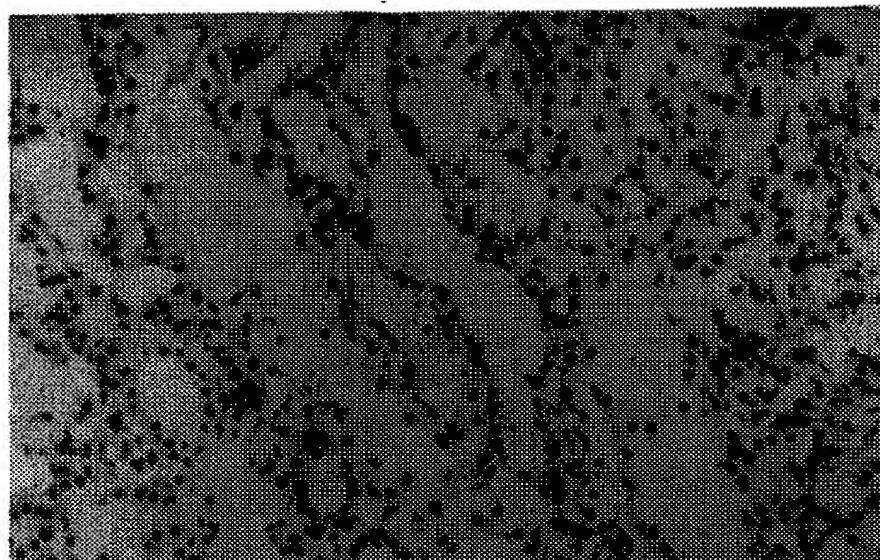
Lightfield

**FIG. 7A**



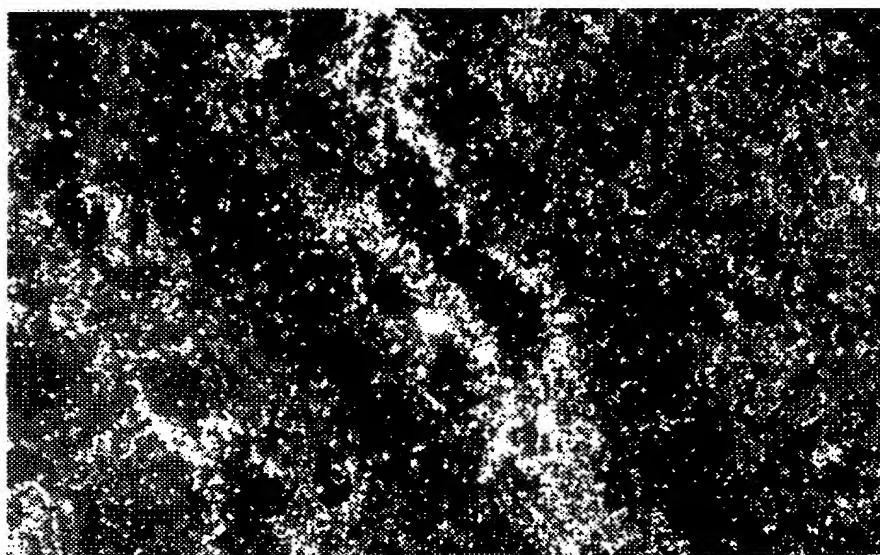
Darkfield

**FIG. 7B**



Lightfield

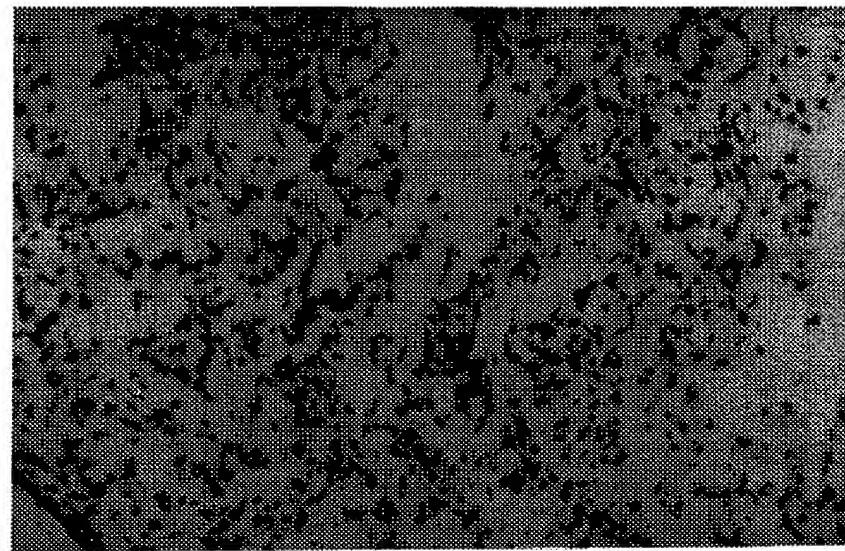
**FIG.8A**



Darkfield

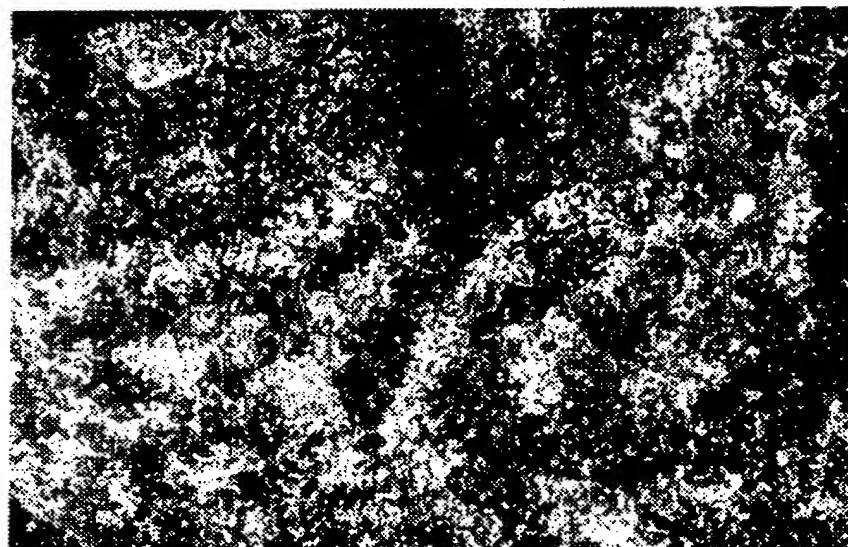
**FIG.8B**

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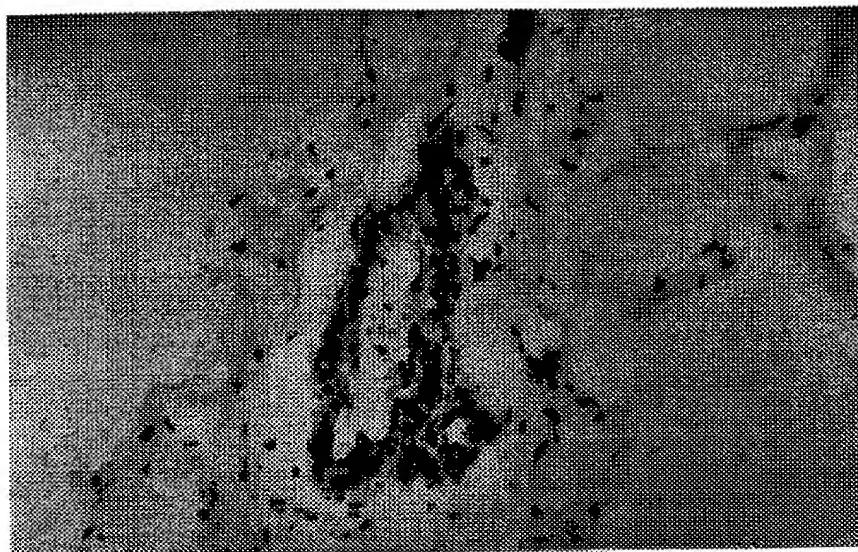
Lightfield

**FIG.9A**

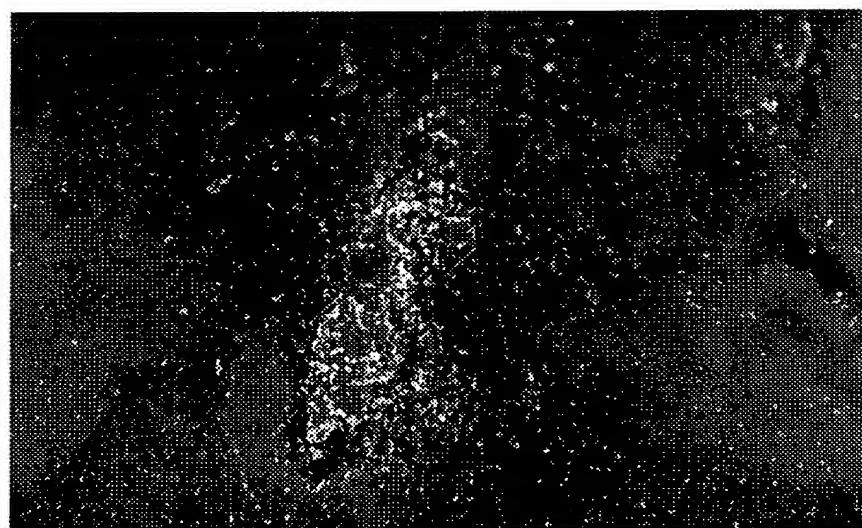


Darkfield

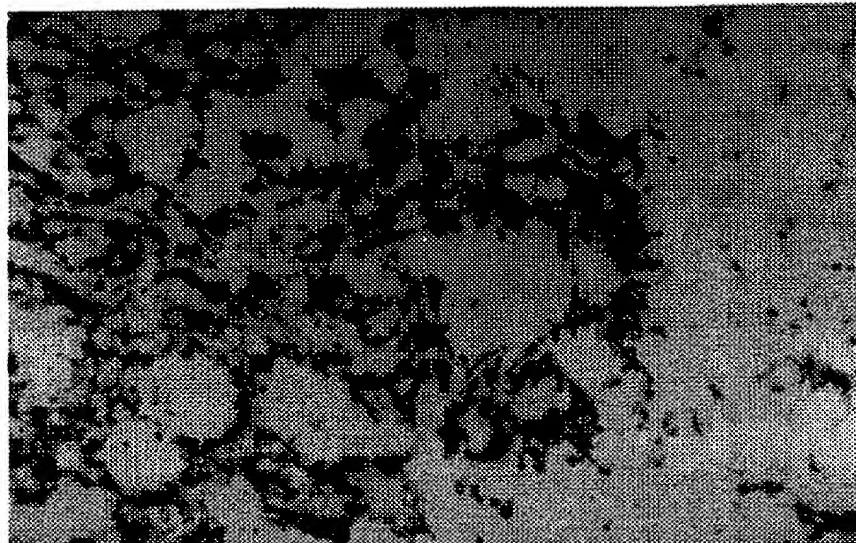
**FIG.9B**



**FIG.10A**

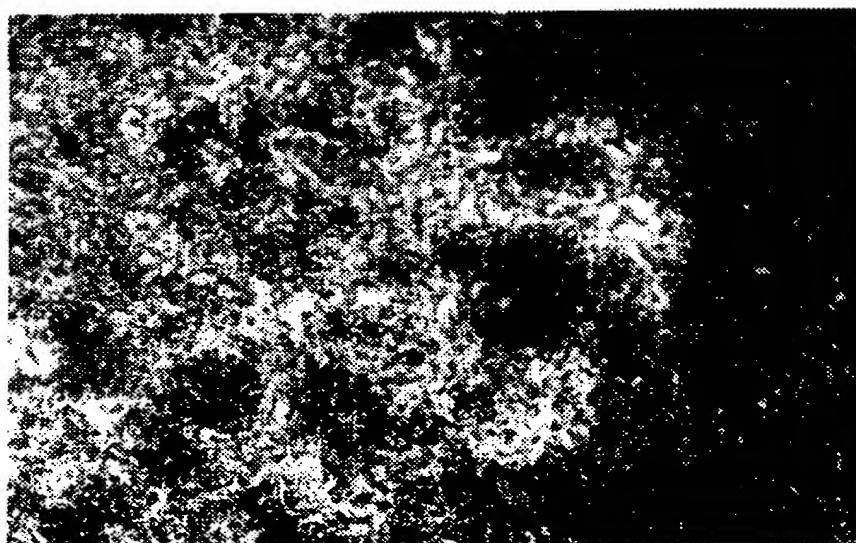


**FIG.10B**



Lightfield

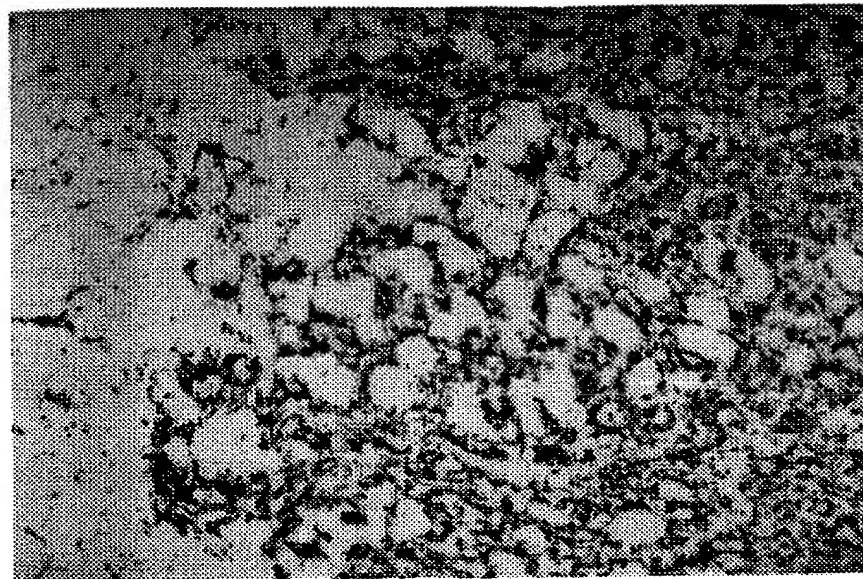
FIG.11A



Darkfield

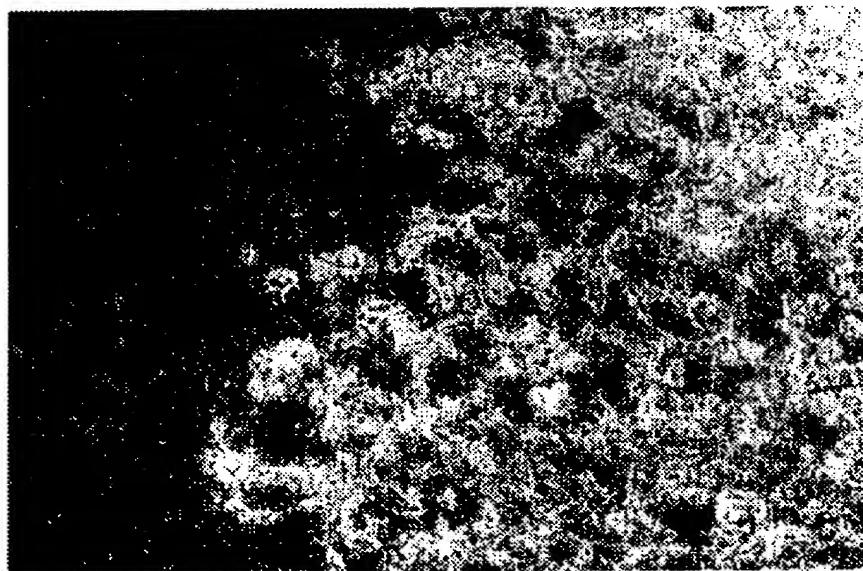
FIG.11B

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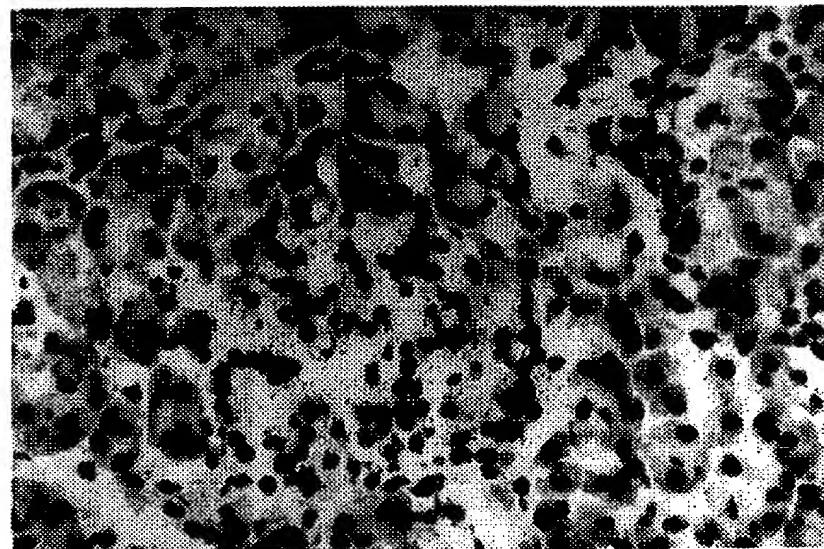
Lightfield

**FIG.12A**



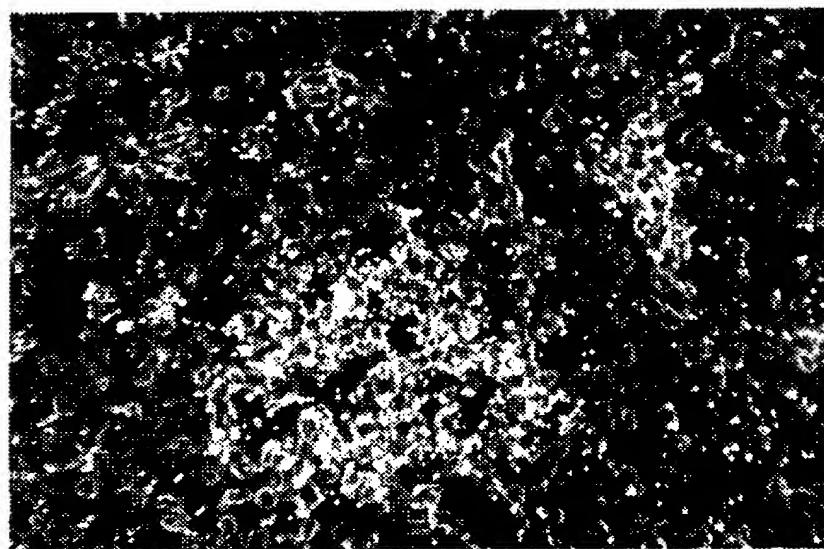
Darkfield

**FIG.12B**



Lightfield

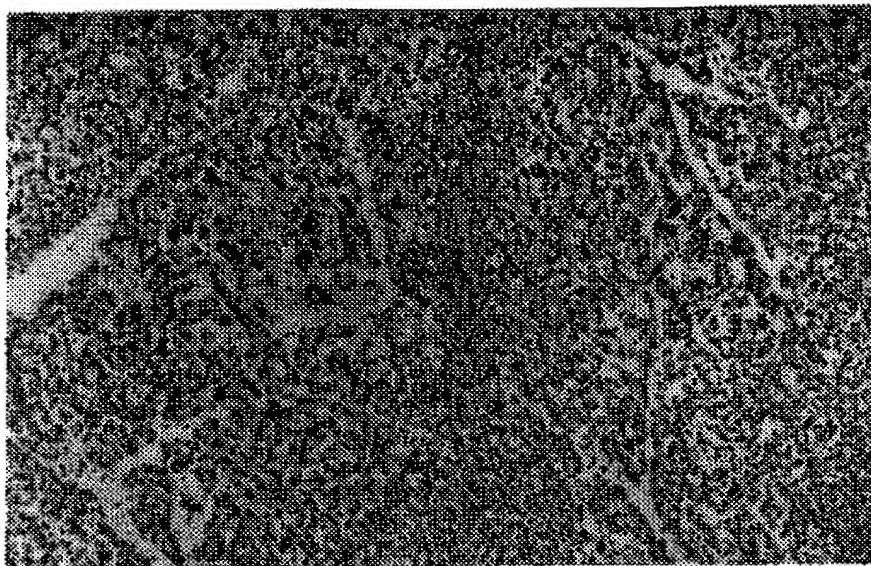
FIG.13A



Darkfield

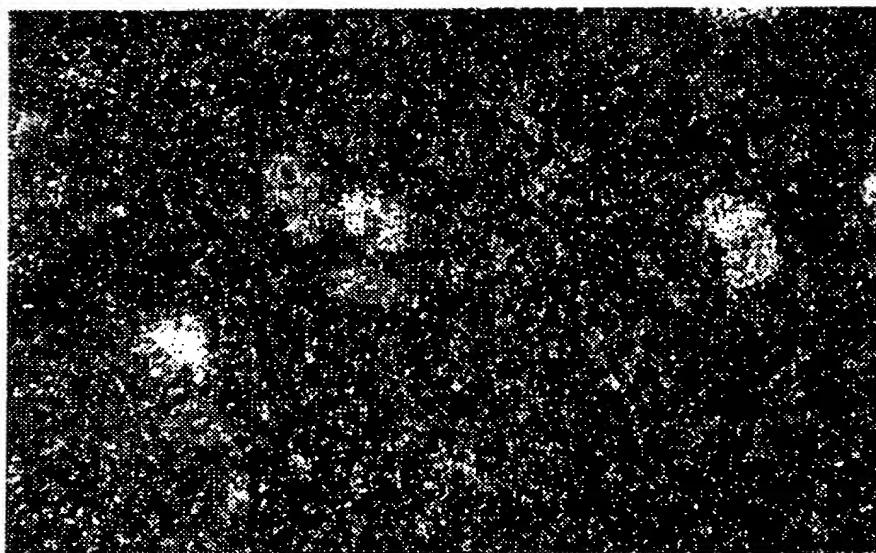
FIG.13B

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Lightfield

FIG. 14A



Darkfield

FIG. 14B

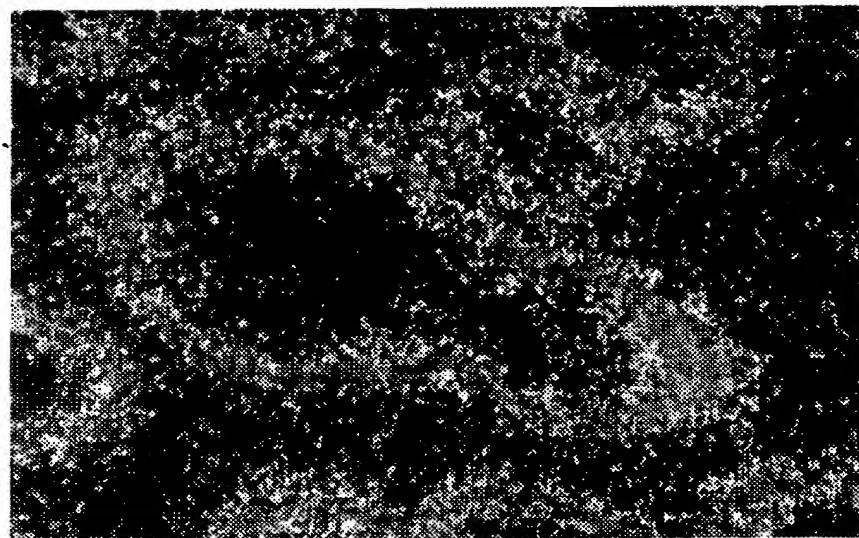


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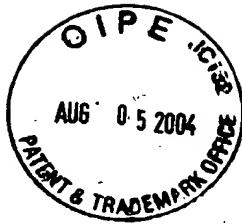
Lightfield

FIG. 15A



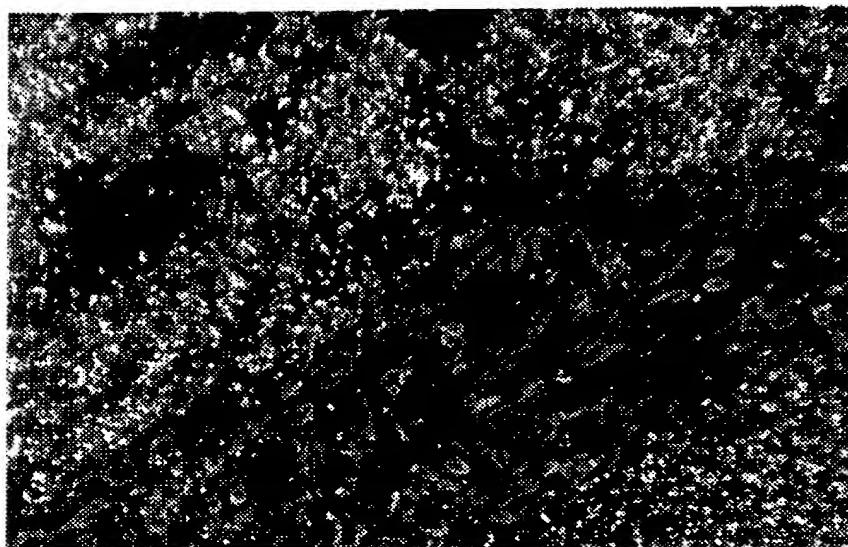
Darkfield

FIG. 15B



Lightfield

FIG.16A



Darkfield

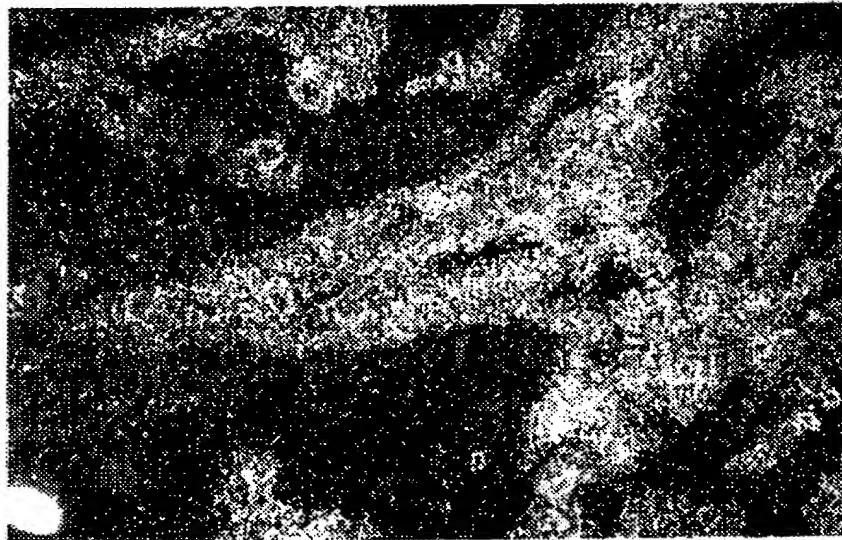
FIG.16B

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Lightfield

FIG.17A



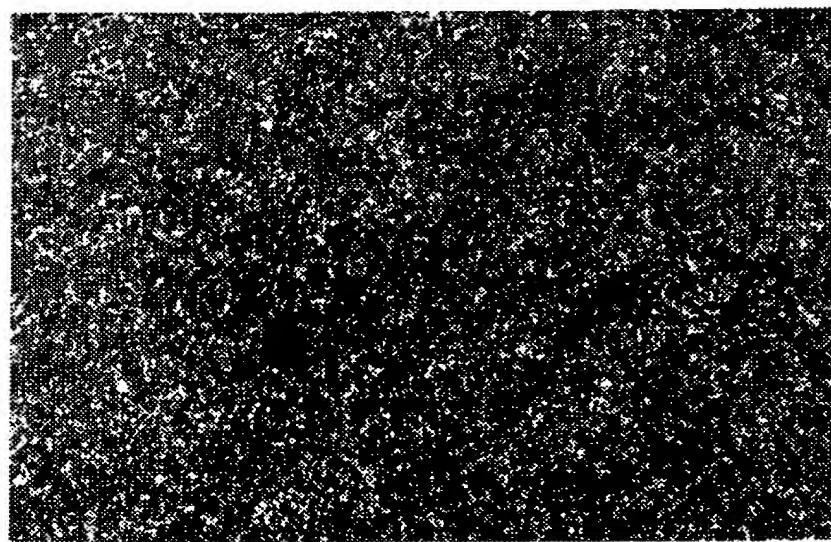
Darkfield

FIG.17B



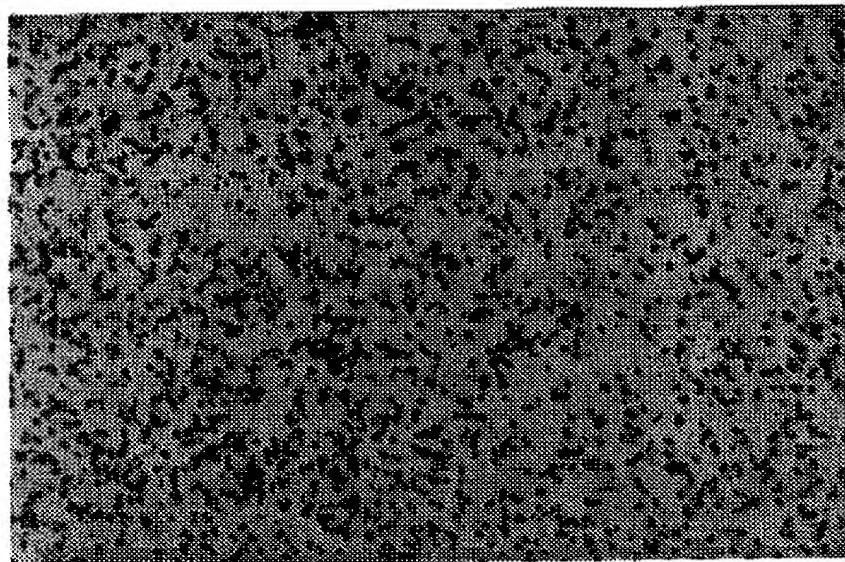
Lightfield

FIG.18A



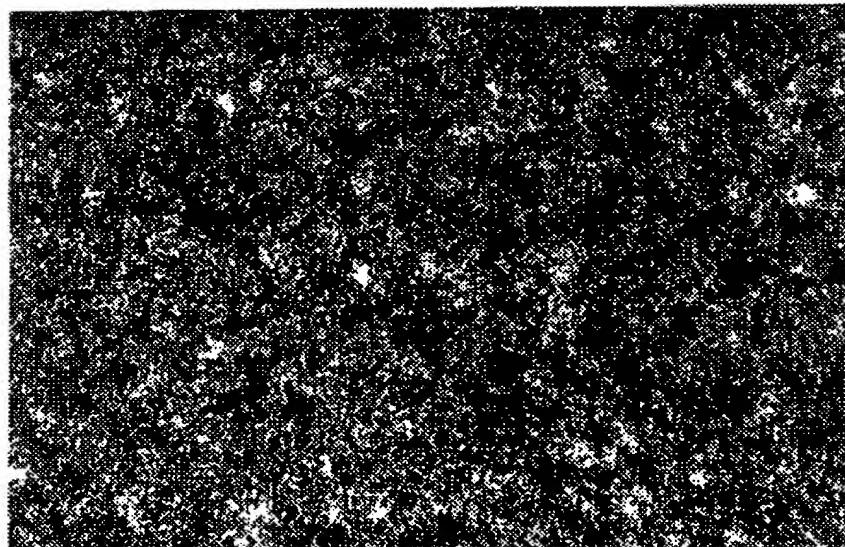
Darkfield

FIG.18B



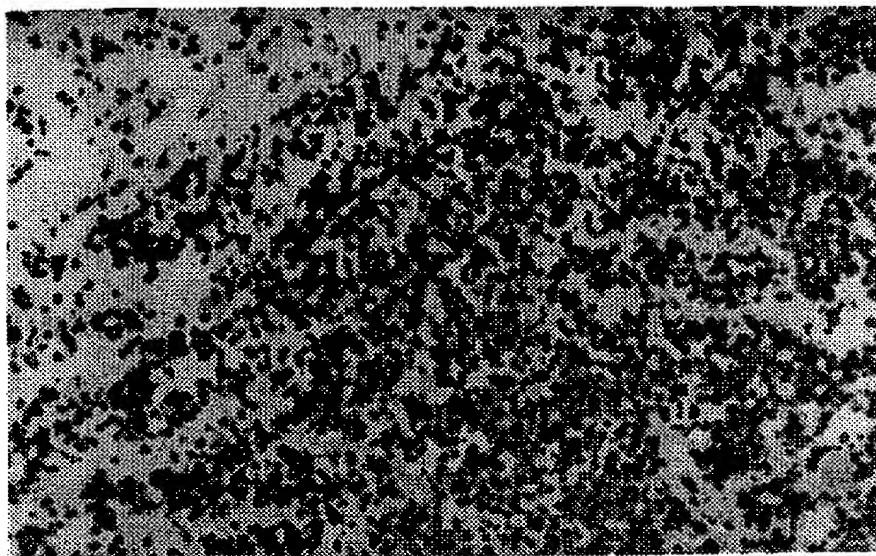
Lightfield

FIG.19A



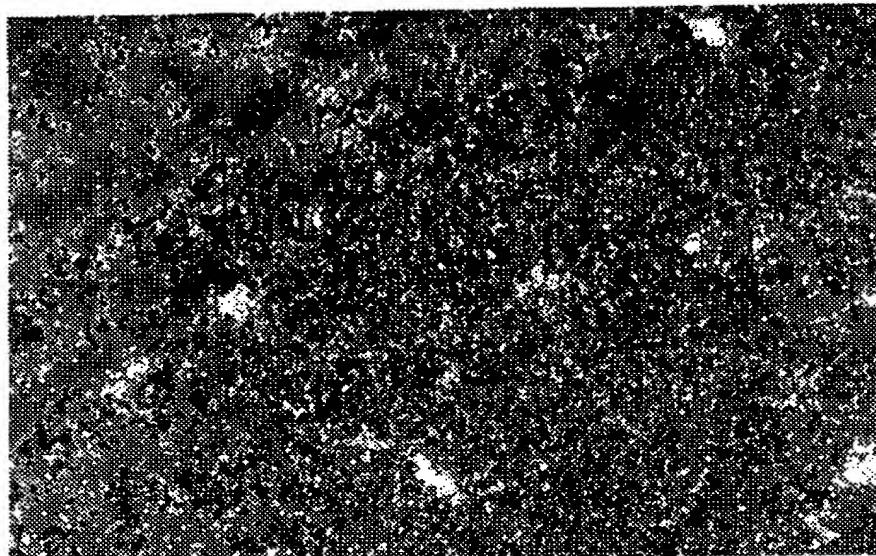
Darkfield

FIG.19B



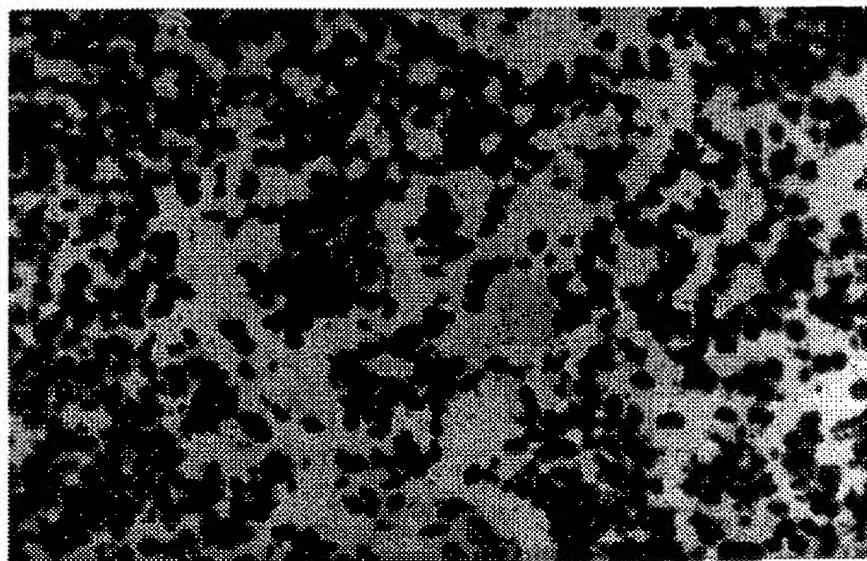
Lightfield

**FIG. 20A**



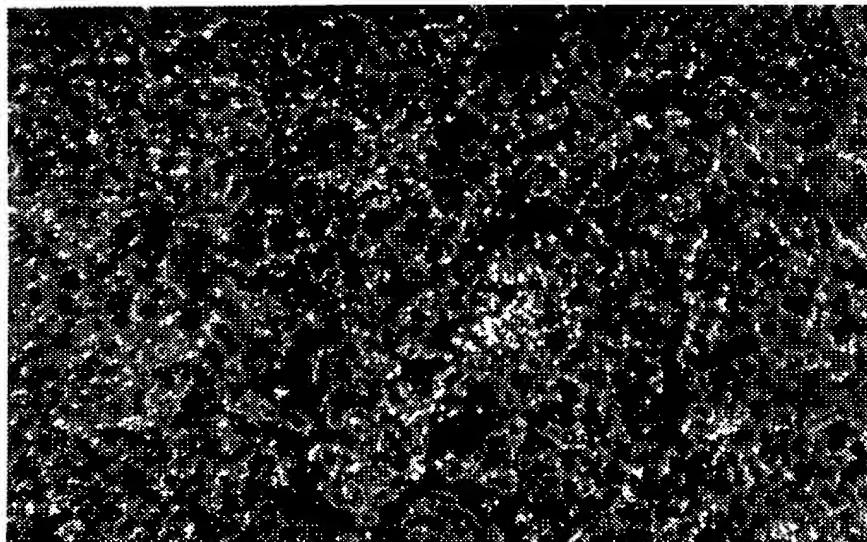
Darkfield

**FIG. 20B**



Lightfield

FIG.21A



Darkfield

FIG.21B